



SEQUENCE LISTING

<110> Kornbluth, Richard S

<120> Multimeric forms of CD40L and other TNF family members

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<141> 1998-12-08

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<170> PatentIn Ver. 2.1

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<222> (88)..(799)

<223> Mature murine surfactant protein D including hub region, collagenous portion and neck, but excluding carbohydrate recognition domain (CRD)

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<223> Human CD40 ligand extracellular region, including stalk.

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<223> Signal peptide from murine surfactant protein D

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<222> (32)..(1444)

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<223> Description of Artificial Sequence: Murine surfactant protein D (without the CRD) fused to

the extracellular portion of human CD40L

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<301> Spriggs, Melanie K.
Armitage, Richard J.
Strockbine, L
Clifford, K N.
Macduff, B M.
Sato, T A.
Maliszewski, C R.
Fanslow, William C.

<302> Recombinant human CD40 ligand stimulates B cell
proliferation and immunoglobulin E secretion.

<303> J. Exp. Med.

<304> 176

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<306> 1543-1550

<307> 1992

<313> 801 TO 1600

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White, R A.

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the extracellular portion of human CD40L

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<301> Anderson, D M.
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Dougall, W C.
<302> A homologue of the TNF receptor and its ligand enhance
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<303> Nature
<304> 390

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Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
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<223> Mature murine surfactant protein D including hub region, collagenous portion, and neck, but excluding carbohydrate recognition domain (CRD)

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<303> J. Immunol.

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<302> Molecular and biological characterization of a murine ligand for CD40

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agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa					
388					
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu					
	105		110		115
ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt					
436					
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly					
120			125		130
cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg					
484					
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met					
		140		145	150
caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga					
532					
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg					
		155		160	165
ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga					
580					
Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly					

170	175	180
cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc 628		
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro 185 190 195		
cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa 676		
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys 200 205 210 215		
ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag 724		
Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu 220 225 230		
gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat 772		
Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr 235 240 245		
cag aaa gct gca ttg ttc cct gat ggc cat aga aga ttg gat aag gtc 820		
Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val 250 255 260		
gaa gag gaa gta aac ctt cat gaa gat ttt gta ttc ata aaa aag cta 868		
Glu Glu Glu Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu 265 270 275		
aag aga tgc aac aaa gga gaa gga tct tta tcc ttg ctg aac tgt gag 916		
Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu 280 285 290 295		
gag atg aga agg caa ttt gaa gac ctt gtc aag gat ata acg tta aac 964		
Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn 300 305 310		
aaa gaa gag aaa aaa gaa aac agc ttt gaa atg caa aga ggt gat gag 1012		
Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu 315 320 325		
gat cct caa att gca gca cac gtt gta agc gaa gcc aac agt aat gca 1060		
Asp Pro Gln Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala		

330	335	340
gca tcc gtt cta cag tgg gcc aag aaa gga tat tat acc atg aaa agc		
1108		
Ala Ser Val Leu Gln Trp	Ala Lys Lys Gly Tyr	Tyr Thr Met Lys Ser
345	350	355
aac ttg gta atg ctt gaa aat ggg aaa cag ctg acg gtt aaa aga gaa		
1156		
Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu		
360	365	370 375
gga ctc tat tat gtc tac act caa gtc acc ttc tgc tct aat cgg gag		
1204		
Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu		
	380	385 390
cct tcg agt caa cgc cca ttc atc gtc ggc ctc tgg ctg aag ccc agc		
1252		
Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser		
	395	400 405
att gga tct gag aga atc tta ctc aag gcg gca aat acc cac agt tcc		
1300		
Ile Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser		
	410	415 420
tcc cag ctt tgc gag cag cag tct gtt cac ttg ggc gga gtg ttt gaa		
1348		
Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu		
	425	430 435
tta caa gct ggt gct tct gtg ttt gtc aac gtg act gaa gca agc caa		
1396		
Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln		
440	445	450 455
gtg atc cac aga gtt ggc ttc tca tct ttt ggc tta ctc aaa ctc		
1441		
Val Ile His Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu		
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1477		

<210> 6

<211> 470

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Murine
surfactant protein D (except CRD) fused to the
extracellular domain of murine CD40 ligand

<400> 6

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			20					25					30		
Thr	Cys	Thr	Leu	Val	Met	Cys	Ser	Pro	Thr	Glu	Asn	Gly	Leu	Pro	Gly
		35					40					45			
Arg	Asp	Gly	Arg	Asp	Gly	Arg	Glu	Gly	Pro	Arg	Gly	Glu	Lys	Gly	Asp
	50					55					60				
Pro	Gly	Leu	Pro	Gly	Pro	Met	Gly	Leu	Ser	Gly	Leu	Gln	Gly	Pro	Thr
65					70					75					80
Gly	Pro	Val	Gly	Pro	Lys	Gly	Glu	Asn	Gly	Ser	Ala	Gly	Glu	Pro	Gly
				85					90					95	
Pro	Lys	Gly	Glu	Arg	Gly	Leu	Ser	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Ile
			100					105					110		
Pro	Gly	Pro	Ala	Gly	Lys	Glu	Gly	Pro	Ser	Gly	Lys	Gln	Gly	Asn	Ile
		115					120					125			
Gly	Pro	Gln	Gly	Lys	Pro	Gly	Pro	Lys	Gly	Glu	Ala	Gly	Pro	Lys	Gly
	130					135					140				
Glu	Val	Gly	Ala	Pro	Gly	Met	Gln	Gly	Ser	Thr	Gly	Ala	Lys	Gly	Ser
145					150					155					160
Thr	Gly	Pro	Lys	Gly	Glu	Arg	Gly	Ala	Pro	Gly	Val	Gln	Gly	Ala	Pro
				165					170					175	
Gly	Asn	Ala	Gly	Ala	Ala	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Pro	Gln	Gly
			180					185					190		
Ala	Pro	Gly	Ser	Arg	Gly	Pro	Pro	Gly	Leu	Lys	Gly	Asp	Arg	Gly	Val
		195					200					205			
Pro	Gly	Asp	Arg	Gly	Ile	Lys	Gly	Glu	Ser	Gly	Leu	Pro	Asp	Ser	Ala
	210					215					220				
Ala	Leu	Arg	Gln	Gln	Met	Glu	Ala	Leu	Lys	Gly	Lys	Leu	Gln	Arg	Leu
225					230					235					240

Glu	Val	Ala	Phe	Ser	His	Tyr	Gln	Lys	Ala	Ala	Leu	Phe	Pro	Asp	Gly			
				245					250					255				
His	Arg	Arg	Leu	Asp	Lys	Val	Glu	Glu	Glu	Val	Asn	Leu	His	Glu	Asp			
			260					265					270					
Phe	Val	Phe	Ile	Lys	Lys	Leu	Lys	Arg	Cys	Asn	Lys	Gly	Glu	Gly	Ser			
		275					280					285						
Leu	Ser	Leu	Leu	Asn	Cys	Glu	Glu	Met	Arg	Arg	Gln	Phe	Glu	Asp	Leu			
	290					295					300							
Val	Lys	Asp	Ile	Thr	Leu	Asn	Lys	Glu	Glu	Lys	Lys	Glu	Asn	Ser	Phe			
305					310					315					320			
Glu	Met	Gln	Arg	Gly	Asp	Glu	Asp	Pro	Gln	Ile	Ala	Ala	His	Val	Val			
				325					330					335				
Ser	Glu	Ala	Asn	Ser	Asn	Ala	Ala	Ser	Val	Leu	Gln	Trp	Ala	Lys	Lys			
			340					345					350					
Gly	Tyr	Tyr	Thr	Met	Lys	Ser	Asn	Leu	Val	Met	Leu	Glu	Asn	Gly	Lys			
		355					360					365						
Gln	Leu	Thr	Val	Lys	Arg	Glu	Gly	Leu	Tyr	Tyr	Val	Tyr	Thr	Gln	Val			
	370					375					380							
Thr	Phe	Cys	Ser	Asn	Arg	Glu	Pro	Ser	Ser	Gln	Arg	Pro	Phe	Ile	Val			
385					390					395					400			
Gly	Leu	Trp	Leu	Lys	Pro	Ser	Ile	Gly	Ser	Glu	Arg	Ile	Leu	Leu	Lys			
				405					410					415				
Ala	Ala	Asn	Thr	His	Ser	Ser	Ser	Gln	Leu	Cys	Glu	Gln	Gln	Ser	Val			
			420					425					430					
His	Leu	Gly	Gly	Val	Phe	Glu	Leu	Gln	Ala	Gly	Ala	Ser	Val	Phe	Val			
		435					440					445						
Asn	Val	Thr	Glu	Ala	Ser	Gln	Val	Ile	His	Arg	Val	Gly	Phe	Ser	Ser			
	450					455					460							
Phe	Gly	Leu	Leu	Lys	Leu													
465					470													